Towards Identifying Biological Research Articles in Computer-Aided Biomimetics

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Abstract. When solving engineering problems through biomimetic design, a lack of knowledge of biology often impedes the translation of biological ideas into engineering principles. Specific challenges are the identification, selection and abstraction of relevant biological information. The use of engineering terminology to search for relevant biological information is hypothesised to contribute to the adventitious character of biomimetics. Alternatively, a holistic approach is proposed where a division is made between the analysis of biological research papers and the decomposition of the engineering problem. The aim of a holisitic approach is to take into account the importance of context during analogical problem solving and provide a theoretical framework for the development of Computer-Aided Biomimetics (CAB) tools. Future work will focus on the development of tools that support engineers during the analysis of biological research papers and modelling of biological systems by providing relevant biological knowledge.

Keywords: Biomimetics, Computer-Aided Biomimetics (CAB), trade-offs, problem-solving

1 Introduction

Biomimetics aims to solve engineering problems through abstraction, transfer and application of knowledge from biological systems, processes, materials etc. (Fayemi et al., 2014). Over the last decades research in biomimetics has rapidly expanded in engineering and related subjects, such as robotics and materials sciences (Lepora et al., 2013). However, while a plethora of biomimetics design methods and tools have been proposed, solving engineering problems through biomimetics remains adventitious and serendipitous (Jacobs et al., 2014)(Vincent, 2016)(Wanieck et al., 2017). Figure 1 visualizes which steps differentiate a generic biomimetics process from a generic problem solving process (Fayemi et al., 2014). Besides abstraction, transfer and application, there are differences in the generation and the selection of alternative solutions. Importantly, the (1) identification of possible candidates of biological models, (2) the selection of the relevant models and (3) their abstraction may be expected to take place primarily in the biological domain. Exactly these steps - identifying, selecting and abstracting biological knowledge relevant to a given engineering prob-

lem - are challenging for someone who is not familiar with biology (Vattam & Goel, 2013a)(Fayemi et al., 2015a).

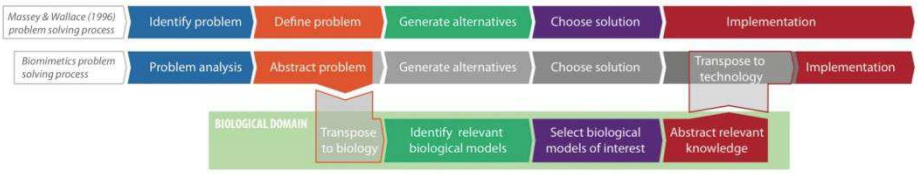

Fig. 1. Generic sequential classical problem solving process (Massey & Wallace, 1996) and biomimetics problem solving process. Based on (Fayemi et al., 2014).

The most common approach to support the steps of identification, selection and abstraction is through the application of what can be regarded as the 'function bridge' (Helfman Cohen & Reich, 2016), where engineering functions are used to classify and describe biological systems. However, the notions of functions in engineering is not the same as that in biology (Perlman, 2009)(Artiga, 2016). Although both artefactual and biological systems may be explained in terms of function, the latter are characterised by dynamic, cyclic, hierarchical processes that rely on information from various systemic levels. Fundamental differences between biology and engineering (Fish et al., 2014) therefore complicate the automated extraction of engineering information from biological texts (Mizoguchi & Borgo, 2016).

During the manual abstraction step, a lack of biological knowledge often leads to wrong interpretations or oversimplification of biological functions (Stricker, 2006)(Helms et al., 2009). Understanding why a biological system is organised as it is, has been obscured through changing environmental conditions and evolutionary requirements. Therefore, Fayemi et al. (2015b) argue that function is not a suitable starting point for the identification and selection of potential biological analogies, as well as for abstraction. Computer-Aided Biomimetics (CAB) tools aim to support manual abstraction of engineering information from biological texts, by extracting and providing within-domain biological information.

To overcome the pitfalls inherent in the use of functions, our research proposes to use trade-offs as a starting point for identification, a central concept in biology that indicates a dialectical relation between traits (Garland, 2014). At a sufficiently high abstraction level, technical and biological trade-offs may be mapped to one another (Vincent, 2016). Trade-offs provide an initial mapping that may be expected to require further filtering to select candidate biological systems. Validating abstractions of biological systems requires contextual knowledge, such as environmental interactions and properties of e.g. biological structures and materials (Kaiser et al., 2014).

The following section 2 introduces the challenges of CAB according to literature. Section 3 elaborates on the use of engineering terminology to overcome these challenges and section 4 emphasises the importance of context and analysis of context. Section 5 introduces the proposed approach to CAB, which requires future work to

focus on relevant computational techniques such as knowledge graphs and relation extraction.

2 CAB requirements according to literature

Several approaches based on the use of databases have been proposed that aim to support engineers through the provision of biological knowledge presented in a terminology that is easy to understand for engineers (Vattam et al., 2010)(Sartori et al., 2010). The most well-known example is AskNature (Deldin & Schuhknecht, 2014), which was found to increase novelty of generated solutions without decreasing the technical feasibility (Vandevenne et al., 2016a). However, considering the large amount of documented biological knowledge (Vandevenne et al., 2016b), manually created databases will never be exhaustive. Due to this inherent limitation on size, and because entering new cases into a database can be arbitrary and effortful, methods and algorithms aimed at supporting biomimetics should be scalable (Vandevenne, 2011).

Approaches that apply Natural Language (NL) analysis can alleviate the inherent limitations of manually created databases by taking advantage of existing repositories of biological knowledge. Shu & Cheong (2014) explored NL analysis for biomimetics using an introductory course book to biology, but the scalability of this approach towards larger repositories remains to be proven. Recent efforts use biological research papers (Kaiser et al., 2014) to automate annotation of biological texts in engineering terminology (Rugaber et al., 2016) and improve the identification of relevant analogies using latent semantics (Vandevenne et al., 2016b). The underlying assumption of this approach is that biological research papers comprehensively cover all documented biological knowledge and describe up-to-date specific expert knowledge (Kaiser et al., 2012)(Vandevenne et al., 2011).

When searching for relevant biological research papers, the main challenges are finding, recognising and understanding relevant information sources (Vattam & Goel, 2011)(Vattam & Goel, 2013b). These challenges correspond to the steps of identification, selection and abstraction of biological models as shown in figure 1, and take place in the biological domain. Familiarity with biology and biological terminology eases these challenges. On the other hand, a lack of biological knowledge impedes abstraction (Helfman Cohen & Reich, 2016) and problem solving in general. Accordingly, a common finding in literature is that a holistic, iterative approach benefits biomimetics (Kruiper et al., 2016).

Regarding the transfer and implementation steps, a variety of models have been proposed to represent biological knowledge for biomimetics, e.g. SAPPhIRE models (Chakrabarti et al., 2014), a Living System Theory approach (Fayemi et al., 2015b) and Structure-Behaviour-Function models (Rugaber et al., 2016). Although differences exist between these, each type of model may be expected to be useful in abstracting and transferring knowledge (Durand et al., 2015). The process of modelling itself helps rationalising thought and developing understanding (Schön, 1983)(Brereton, 2004). Table 1 provides an overview of the recommendations for CAB tools according to literature.

Table 1. Overview of the challenges Computer-Aided Biomimetics tools should aim to overcome and the related themes of common mistakes and recurring findings. Based on (Kruiper et al., 2016) and Vattam & Goel (2011, 2013a).

Themes	Challenges
Scalability	Ability to integrate large amounts of biological knowledge to support biomimetics processes
Formalisation Transfer impediments Validation Analogies	**Identification** of possibly relevant information sources, out of all existing information sources, based on a query. Reduce the amount of time spent browsing query results.
Transfer impediments Validation Analogies	**Selection** of information sources that seem most relevant within the set of possible information sources. Improve the ability to recognize the content in the results.
Transfer impediments Validation Abstraction	**Abstraction** in biomimetics is "*the process of refining the biological knowledge (design solutions) to some working principles, strategies or representative models that explain the biological solution and could be further transferred to the target application*" (Helfman Cohen & Reich, 2016). This encompasses moving from 'understanding the biological terminology' towards 'using appropriate methods for describing and decoding biological principles.'
Holistic Approach	Ability to alternate between problem decomposition and analogical reasoning, simultaneously expanding the designers' knowledge required for validation.

3 Engineering terminology in CAB

Considering the desired scalability of CAB tools an approach that applies NL analysis of biological research papers seems reasonable. However, assuming that biology research papers are written using domain-specific terminology, this approach limits the use of engineering terminology in identifying relevant biological information. Reasons include the different words used in biological and engineering research papers, as well as differences in the semantic meaning of words and core concepts like function as explained earlier.

3.1 Differences in biological and engineering terminology

Nagel (2014) notes that domain knowledge is required to understand biological *'flows'* (as cited from Pahl & Beitz, 2007) of materials, energy and information. Having to look up each term is tedious and disrupts the thought process, or rather the *'flow'* (Csikszentmihalyi, 1990). Figure 2 displays a word cloud that provides some intuition on the type of terms that engineers may not be familiar with. Crucially, unknown terms will not be useful during identification or selection of biological re-

search papers. Terminological differences between biological texts and engineering texts therefore render direct keyword-based search inadequate (Vattam & Goel, 2011).

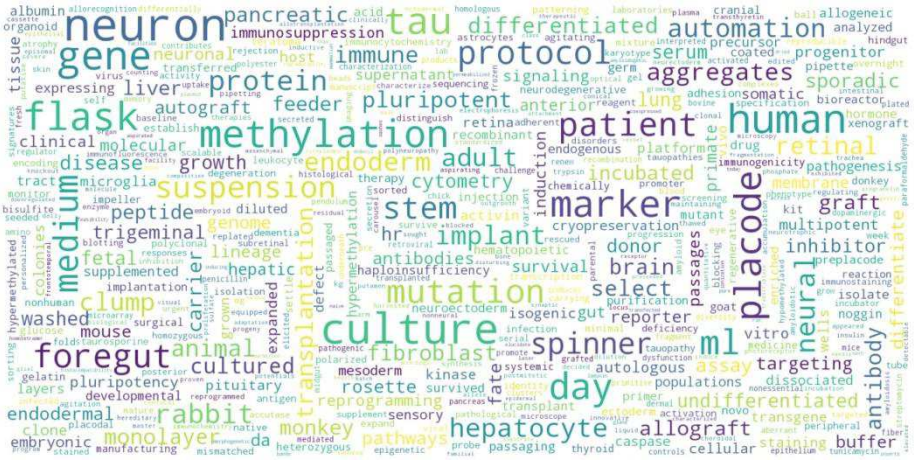

Fig. 2. *Word cloud generated from eleven biological research papers. Two sets of eleven research papers belonging to the biological and engineering domain respectively were used from the Elsevier OA-STM-corpus (2015). The words in the vocabulary represent all words in the biology papers, minus those words occurring in the engineering papers. Although the sets of documents are limited in size and do not cover all topics of both domains, the resulting terms provide an intuition of biological terminology that engineers may not be familiar with, such as haploinsufficiency, hepatocyte, allograft, placode, microglia, caspase etc.*

Vattam & Goel (2011) suggest that, in absence of biological knowledge, selection is specifically limited to *semantic similarity*. However, similarity and relevance of higher-order relations are neglected, e.g. taxonomical and entity-relations. *Semantic similarity* here is the overlap in number of similar words used in a search query and found in the retrieved documents. In this sense, *semantic similarity* is a measure of frequent association without necessarily overlapping in the semantic meaning of the words.

To improve the identification and selection of relevant biological systems Vattam & Goel (2013b) suggest annotating biological research papers with engineering terminology, which may also ease the understanding of biological analogies. Rugaber et al. (2016) describe a CAB system that automatically annotates biological research papers with Structure-Behaviour-Function (SBF) models. Functions are represented in verb-object format and extracted by matching functional verbs from a controlled vocabulary that is based on the Functional Basis (Hirtz et al., 2002) and the Biomimicry Taxonomy of AskNature. Behaviours are extracted using syntactic patterns that are a subset of the patterns by Khoo et al. (1998, 2000). Structures are terms matched against a vocabulary of biological structures based on part of an ontology for biomimetics – a formal and explicit representation of knowledge – created by Vincent (2014, 2016).

The assumption by Rugaber et al. (2016) is that SBF models can robustly represent biological systems. However, automatically extracted annotations will only be as useful as the type and quality of information they model. Using vocabularies of engineering functions to annotate and retrieve biological research papers does not extend key-word based search. The added value then lies in the quality of extracted behaviours and structures – the systemic context of the functions.

3.2 Different semantics and core concepts

While SBF models may be used to represent a biological system, differences in the semantic meaning of words introduce an important issue in automatically extracting engineering information from biological research papers. Vandevenne et al. (2016b) circumvent this problem by clustering terms frequently occurring together in documents, either in the biological or engineering domain. The resulting manually labelled concepts, 300 so-called Organism Aspects, are extracted from 8,011 biological research papers. In a previous work, the authors extract 300 Product Aspects from 155,000 patents. Cross-domain associations are provided, based on the similarity between the concept vectors, representing the occurrence of domain-specific terms.

The cross-domain associations enable the matching of *semantically similar* groups of biological terms to groups of engineering terms. Based on the terms occurring in biological research papers, the papers can then be annotated with *semantically similar* engineering concepts. Therefore, using pre-specified engineering terminology – the Product Aspects – relevant biology research papers can be identified. A keyword like the verb 'to float' may, for example, return a paper that mentions buoyancy several times. However, the occurrence of *semantically similar* words does not necessarily improve the selection, or indicate the existence, of analogies relevant to the engineering problem.

In analogical problem solving, relations between individual parts of a system are dominant aspects (Markman & Gentner, 1983)(Gentner & Kurtz, 2006)(Verhaegen, 2011). Representations that capture systemic relations, e.g. functional representations like SBF models, can thus support analogical reasoning. Functions in general may be used to capture analogies between individual parts of biological systems and engineering systems. The usefulness of such analogous functions in Design-by-Analogy is reflected in the commonly used 'function-bridge' in biomimetics. However, in the case where CAB systems focus on text-processing of biological research papers fundamental differences between the semantic meaning of concepts like biological and engineering functions have to be taken into account. The same applies to the semantic meaning of words associated to such concepts; well-known functional verbs for example may not convey the same meaning in engineering and biology (Nagel, 2014).

From a teleological point of view, biological functions and engineering functions are different (Artiga, 2016). To denote the intention-neutrality of biological functions, a static view of a biological process may be considered a *role* within the context of a system (Chandrasekaran et al, 2000). Generally a function may be regarded as the capacity to perform a behaviour within a given context (Mizoguchi & Borgo, 2016).

4 Context and analysis

Kaiser et al. (2014) show that verbs associated with engineering functions are not always present in biological research papers. In case functional terms are found in biological research papers, they often co-occur with terms describing environmental characteristics that may influence the function. To exemplify the importance of context, consider the self-cleaning functionality known as the *lotus effect*. This function, or rather property, exhibited by a variety of plants and insects, is based on superhydrophobicity that can be introduced through a variety of microscopic structures (Meyers, 2015)(Barthlott & Neinhuis, 1997). In plant leaves, these structures are mainly formed by epicuticular wax crystalloids, of which the shape is determined by specific compounds in the wax. In contrast to marsh and water plants the wettability of surfaces is noted to be of little importance to plants originating from Mediterranean-type habitats or subtropical regions. "*Here, trichomes or waxes are most probably involved in the regulation of the radiation budget and, therefore, indirectly in temperature control"* (Neinhuis & Barthlott, 1997). Thus, although the self-cleaning functionality of surfaces may be attributed to superhydrophobicity of a surface, this functionality depends on a variety of traits at multiple hierarchical levels. Furthermore, depending on external properties, the same trait can vary statically over phylogenetic distance or dynamically over ecological similarity. The differences between the surface structures found on leaves of various plant species are strongly correlated to their wettability and thus the self-cleaning property.

On the other hand, over-reliance on e.g. the self-cleaning function of superhydrophobic surfaces may obscure other functionalities based on the same principle. Superhydrophobicity can also enable floating capacity, e.g. in water striders legs (Feng et al., 2007). Furthermore, Cicada orni combine hydrophobicity with the anti-reflective property known as the moth-eye effect in a multi-layered nanostructure (Dellieu et al., 2014). Similarly the swim bladder of a fish is well known as an organ that provides buoyancy while swimming underwater. Simultaneously, the swim bladder is a structure that includes a lumen. Some species of fish use a swim bladder to improve precision in sensing water pressure (Taylor, 2010) and some to support sound production and hearing (Millot et al., 2011). The same structure or process may thus be involved in various functional properties.

The contextual variables on which a functional property depends can greatly influence the functional capacity. While an engineer may be interested only in a single *'function'* of a biological system, neglecting context often renders a direct transfer to engineering impossible (Inkermann et al., 2011). Due to the tight coupling between properties, biological systems can hardly be seen as parts associated with functions (Fayemi et al., 2015b). Considering knowledge transfer as the goal of modelling biological systems in terms of technical systems, searching for biological research papers using engineering functions requires that some form of abstraction is already performed.

5 Proposed CAB design approach

The biological and engineering terminology and semantics are inherently different. As a result, the use of engineering terminology to search over or automate annotation of biological texts is unreliable. While engineering functions may suffice to describe a design requirement independent of context, biological functions are tightly interrelated to context and a direct transfer may not be possible. Accordingly, the transfer of knowledge between both domains is noted to actually happen between representations of the biological and technical system (Sartori et al., 2010). Therefore, as displayed in figure 3, the proposed approach to CAB focuses on supporting engineers in representing biological systems of interest.

TRIZ, a set of tools for solving engineering problems creatively, has received a fair amount of attention in biomimetics (Vincent & Mann, 2002)(Vincent et al., 2006)(Bogatyrev & Bogatyrev, 2015)(Fayemi et al., 2014)(Vandevenne et al., 2015)(Helfman Cohen & Reich, 2016). TRIZ theory prescribes a high level of abstraction during problem decomposition, e.g. using contradictions to denote a trade-off or dialectic relation between parameters of components in a technical system (Cavallucci et al., 2009). In TRIZ these abstract contradictions can be used to direct an engineer towards abstract solution routes. Similarly, according to Vincent (2016) trade-offs can be used to classify biological solution routes based on the abstract parameters involved. Trade-offs can thus support the identification of relevant biological systems without the need to encode biological information in specific theoretical models. As a result, the proposed approach offers freedom over theoretical models used to represent biological knowledge, but is limited to either highly abstract or biological terminology.

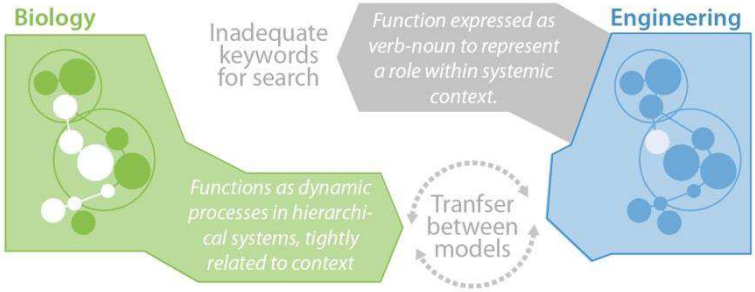

Fig. 3. *Rather than searching for biological research papers using engineering terminology (top: function-bridge), the proposed approach aims to support the modelling of biological systems (bottom: taking context into account).*

In modelling the relations between properties, interdependence exists between (1) the available biological knowledge, (2) the abstraction of engineering knowledge from a source of biological information and (3) the transfer of knowledge to a given engineering application. Hence, as noted in table 1, an iterative approach is beneficial to biomimetics. Using theoretical models to capture contextual variables in various

representations helps developing design understandings (Brereton, 2004). In support of a holistic design process, we propose that CAB tools focus on indicating the relations, semantic concepts and named entities required to understand biological strategies in their respective context.

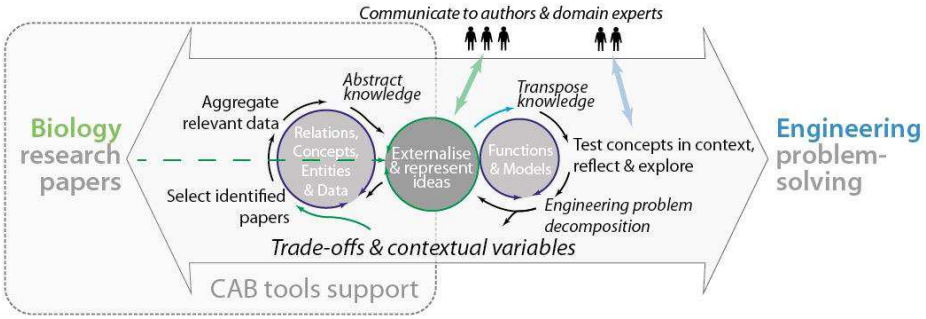

Fig. 4. *Overview of the proposed approach to biomimetics supported by Computer-Aided Biomimetics (CAB) tools. CAB tools here aim to support a holistic, iterative approach to the search for biological data.*

In a holistic biomimetic design process, communicating 'raw' design ideas throughout the design process, as well as intuitive exploration, supports rationalising thought (Wendrich, 2012). Although the search is for analogies, surprising properties and differences may be expected to provide considerable heuristic power in biomimetic problem solving (Bensaude-Vincent, 2011)(Salgueiredo, 2013). Figure 4 displays how cross-domain knowledge transfer is facilitated by a continuous loop of communication, reflection-in-action, reflection-on-action and reflection-in-practice (Schön, 1983). Hence, in the proposed biomimetic design approach the designer is constantly representing domain-specific knowledge to support validation and knowledge transfer. Such iterative externalisation of ideas and the interaction with predetermined or loosely defined constraints leads to novel insights (Wendrich & Kruiper, 2016), without neglecting multi-functionality and interrelations at multiple hierarchical levels. Future work will now implement and aim to validate this approach using the advanced computer tools available to us.

6 Conclusion

Several prevalent challenges in biomimetic problem solving processes are related to a lack of biological knowledge. In overcoming these challenges, computational tools may access the knowledge captured in biological research papers. Using biological research papers as information source limits the use of engineering terminology for search and automated annotation. However, the terminology used in biological research papers captures specific contextual knowledge. Such contextual variables can greatly influence functional capacities of a biological system. Modelling these contextual variables and inter-relations in biological systems leads to understanding the nec-

essary knowledge for abstraction. A holistic approach is proposed that supports iteratively exploring biological information against predetermined engineering constraints.

In the proposed approach Computer-Aided Biomimetics (CAB) tools focus on extracting contextual variables and relation from biological research papers. Specifically relations between individual parts of a system are of interest to analogical problem solving. Various theoretical models may be useful in representing biological systems to support validation and knowledge transfer. Future work will focus on the extraction, retrieval and representation of knowledge in CAB tools to support our approach. The aim is to provide common sense biological background knowledge and identify trade-offs between abstract parameters.

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